

## RAW SEQUENCE LISTING

DATE: 09/24/2003

PATENT APPLICATION: US/10/663,451

TIME: 15:32:21

Input Set : N:\CrF3\RULE60\US10663451.raw.txt

Output Set: N:\CRF4\09242003\J663451.raw

49	Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile Lys Thr Thr Arg	
50		40 45 50
51	gac cga gtg cct aca tat cag tac aac atg aat ttt gaa aag ctg ggc	247
52	Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe Glu Lys Leu Gly	
53		55 60 65
54	aaa tgc atc ata ata aac aac aag aac ttt gat aaa gtg aca ggt atg	295
55	Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys Val Thr Gly Met	
56		70 75 80
57	ggc gtt cga aac gga aca gac aaa gat gcc gag gcg ctc ttc aag tgc	343
58	Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala Leu Phe Lys Cys	
59		85 90 95 100
60	ttc cga agc ctg ggt ttt gac gtg att gtc tat aat gac tgc tct tgt	391
61	Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn Asp Cys Ser Cys	
62		105 110 115
63	gcc aag atg caa gat ctg ctt aaa aaa gct tct gaa gag gac cat aca	439
64	Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu Glu Asp His Thr	
65		120 125 130
66	aat gcc gcc tgc ttc gcc tgc atc ctc tta agc cat gga gaa gaa aat	487
67	Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His Gly Glu Glu Asn	
68		135 140 145
69	gta att tat ggg aaa gat ggt gtc aca cca ata aag gat ttg aca gcc	535
70	Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys Asp Leu Thr Ala	
71		150 155 160
72	cac ttt agg ggg gat aga tgc aaa acc ctt tta gag aaa ccc aaa ctc	583
73	His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu Lys Pro Lys Leu	
74		165 170 175 180
75	ttc ttc att cag gct tgc cga ggg acc gag ctt gat gat ggc atc cag	631
76	Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp Asp Gly Ile Gln	
77		185 190 195
78	gcc gac tcg ggg ccc atc aat gac aca gat gct aat cct cga tac aag	679
79	Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn Pro Arg Tyr Lys	
80		200 205 210
81	atc cca gtg gaa gct gac ttc ctc ttc gcc tat tcc acg gtt cca ggc	727
82	Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser Thr Val Pro Gly	
83		215 220 225
84	tat tac tcg tgg agg agc cca gga aga ggc tcc tgg ttt gtg caa gcc	775
85	Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp Phe Val Gln Ala	
86		230 235 240
87	ctc tgc tcc atc ctg gag gag cac gga aaa gac ctg gaa atc atg cag	823
88	Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu Glu Ile Met Gln	
89		245 250 255 260
90	atc ctc acc agg gtg aat gac aga gtt gcc agg cac ttt gag tct cag	871
91	Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His Phe Glu Ser Gln	
92		265 270 275
93	tct gat gac cca cac ttc cat gag aag aag cag atc ccc tgt gtg gtc	919
94	Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile Pro Cys Val Val	
95		280 285 290
96	tcc atg ctc acc aag gaa ctc tac ttc agt caa tag ccatatcagg	965
97	Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln	

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98          295          300
99      ggtacattct agctgagaag caatgggtca ctcattaatg aatcacattt ttttatgctc 1025
100      ttgaaatatt cagaaattct ccaggatttt aatttcagga aaatgtattg attcaacagg 1085
101      gaagaaactt tctggtgctg tcttttggtc tctgaatttt cagagacttt tttataatgt 1145
102      tattcatttg gtgactgtgt aactttctct taagattaat tttctctttg tatgtctgtt 1205
103      accttgttaa tagacttaat acatgcaaca gaagtgaact ctggagaaaag ctcatggctg 1265
104      tgtccactgc aattgggtgt aacagtggta gagtcatgtt tgcacttggc aaaaagaatc 1325
105      ccaatgtttg acaaaacaca gccaaagggga tattttactgc tctttattgc agaattgtggg 1385
106      tattgagtgt gatttgaatg atttttcatt ggcttagggc agattttcat gcaaaagttc 1445
107      tcatatgagt tagaggagaa aaagcttaat gattctgata tgtatccatc aggatccagt 1505
108      ctggaaaaca gaaaccattc taggtgtttc aacagagggga gtttaataca ggaaattgac 1565
109      ttacatagat gataaaagag aagccaaaca gcaagaagct gttaccacac ccagggttat 1625
110      gaggataatg ggaagagggt tggtttctct tgtccagtag tgggatcatc cagaggagct 1685
111      ggaaccatgg tgggggctgc ctagtgggag ttaggaccac caatggattg tggaaaatgg 1745
112      agccatgaca agaacaaagc cactgactga gatggagtga gctgagacag ataagagaat 1805
113      acctgtctc acctatcctg ccctcacatc ttccaccagc accttactgc ccaggcctat 1865
114      ctggaagcca cctcaccaag gaccttgaa gagcaaggga cagtgaggca ggagaagaac 1925
115      aagaaatgga tgtaagcctg gcccataatg tgaacataag taatcactaa tgctcaacaa 1985
116      tttatccatt caatcattta ttcattgggt tgtcagatag tctatgtatg tgtaaaacaa 2045
117      tctgttttgg ctttatgtgc aaaatctgtt atagctttta aatatatctg gaacttttta 2105
118      gattattcca agccttattt tgagtaaata tttgttactt ttagttctat aagtgaggaa 2165
119      gagtttatgg caaagatttt tggcactttg ttttcaagat ggtgttatct tttgaattct 2225
120      tgataaatga ctgttttttt ctgcctaata gtaactgggt aaaaaacaaa tgttcatatt 2285
121      tattgattaa aaatgtgggt gctt                                     2309
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 26
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: PCR Primer
129 <400> SEQUENCE: 4
130      attggtggtgta acagtggtag agtcat                                     26
132 <210> SEQ ID NO: 5
133 <211> LENGTH: 20
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: PCR Primer
138 <400> SEQUENCE: 5
139      cccttggtctg tgttttgtca                                     20
141 <210> SEQ ID NO: 6
142 <211> LENGTH: 27
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: PCR Probe
147 <400> SEQUENCE: 6
148      ttgcacttgg caaaaagaat cccaatg                                     27
150 <210> SEQ ID NO: 7

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151 <211> LENGTH: 21
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: PCR Primer
156 <400> SEQUENCE: 7
157     caacggattt ggtcgtattg g
158                                     21
159 <210> SEQ ID NO: 8
160 <211> LENGTH: 26
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: PCR Primer
165 <400> SEQUENCE: 8
166     ggcaacaata tccactttac cagagt
167                                     26
168 <210> SEQ ID NO: 9
169 <211> LENGTH: 21
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: PCR Probe
174 <400> SEQUENCE: 9
175     cgcctgggtca ccagggtgc t
176                                     21
177 <210> SEQ ID NO: 10
178 <211> LENGTH: 2006
179 <212> TYPE: DNA
180 <213> ORGANISM: Mus musculus
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (474)...(1496)
184 <400> SEQUENCE: 10
185     agctcagtga ggctgatgtg tactgcacat ttaaaaaaaaa aatcacagga attttcatac
186     aatgaataaa accacaacaa tacatgtaga attggcaggt ggaaaagagc cagcaagggc
187     tcaaaactaat cactcacttt ccctcttcag catagttcaa ccaacagtag cacactttca
188     cctacaaatc ttaaagtagc tccatcaaat ctgcagtttt cacattattg aaaatgtctg
189     tcacataggt acaaatttag aatcatcaca ttatattaca tggctattct aggtcatcta
190     tagatcagat cttagactac agtgattgaa gttcttcgta cagccatcaa aaagggacac
191     atgatcatta cttactgtta gtcacatct aaaggcatga aaaggtttcc tttttttcaa
192     ctgacccaaa cactttaccc caatagtgcc aggttcctc tctgctgctt tga atg
193                                     Met
194                                     1
195     ttc aca gcc caa gtg ttc tca gag tcc ttt aca aaa act gag ttg ctg
196     Phe Thr Ala Gln Val Phe Ser Glu Ser Phe Thr Lys Thr Glu Leu Leu
197           5                10                15
198     ccc tcg acc ctt gcg gag gac gga cgc tgc cgt ggg ctc ctg gcc gcc
199     Pro Ser Thr Leu Ala Glu Asp Gly Arg Cys Arg Gly Leu Leu Ala Ala
200           20                25                30
201     gcc gtg gga acg atg acc gat gat cag gac tgt gct gcg gag ctg gaa
202     Ala Val Gly Thr Met Thr Asp Asp Gln Asp Cys Ala Ala Glu Leu Glu

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203	35	40	45	
204	aag gtg gat tct tcc agc gaa gac gga gtt gac gcc aag cca gac cgc	668		
205	Lys Val Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg			
206	50	55	60	65
207	tcc tct atc atc tcc tct att ctc ttg aag aag aag aga aat gcc tct	716		
208	Ser Ser Ile Ile Ser Ser Ile Leu Leu Lys Lys Lys Arg Asn Ala Ser			
209	70	75	80	
210	gcg ggc ccc gtc agg acc ggc cgg gac cga gtg ccc act tat ctg tac	764		
211	Ala Gly Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr			
212	85	90	95	
213	cgc atg gat ttc cag aag atg ggt aaa tgc atc atc ata aac aac aag	812		
214	Arg Met Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys			
215	100	105	110	
216	aac ttc gac aaa gcg aca ggt atg gac gtc cgg aat ggg acg gac aaa	860		
217	Asn Phe Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys			
218	115	120	125	
219	gat gca ggg gcc ctc ttc aag tgc ttc caa aac ctg ggt ttt gaa gta	908		
220	Asp Ala Gly Ala Leu Phe Lys Cys Phe Gln Asn Leu Gly Phe Glu Val			
221	130	135	140	145
222	acc gtc cac aat gac tgc tct tgt gca aag atg caa gat ctg ctt aga	956		
223	Thr Val His Asn Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Arg			
224	150	155	160	
225	aaa gcc tct gag gag gac cac agc aac tcg gcc tgc ttc gcc tgc gtc	1004		
226	Lys Ala Ser Glu Asp His Ser Asn Ser Ala Cys Phe Ala Cys Val			
227	165	170	175	
228	ctg ctg agc cac ggg gaa gag gac ctg att tac ggg aaa gat ggc gtg	1052		
229	Leu Leu Ser His Gly Glu Glu Asp Leu Ile Tyr Gly Lys Asp Gly Val			
230	180	185	190	
231	aca ccc ata aag gat ctg aca gct cat ttt agg gga gac cga tgc aaa	1100		
232	Thr Pro Ile Lys Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys			
233	195	200	205	
234	acc ctg tta gag aaa ccc aaa ctc ttc ttc att cag gca tgc cga ggg	1148		
235	Thr Leu Leu Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly			
236	210	215	220	225
237	acg gag ctc gac gat gga atc cag gct gac tcg ggg ccc atc aac gac	1196		
238	Thr Glu Leu Asp Asp Gly Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp			
239	230	235	240	
240	att gac gct aat ccc cgc aac aag atc ccg gtg gaa gcc gac ttc ctc	1244		
241	Ile Asp Ala Asn Pro Arg Asn Lys Ile Pro Val Glu Ala Asp Phe Leu			
242	245	250	255	
243	ttt gct tac tcc acg gtt cca ggt tat tac tca tgg agg aac cca ggg	1292		
244	Phe Ala Tyr Ser Thr Val Pro Gly Tyr Tyr Ser Trp Arg Asn Pro Gly			
245	260	265	270	
246	aaa ggc tcc tgg ttt gtg cag gcc ctc tgc tcc atc ctg aat gag cat	1340		
247	Lys Gly Ser Trp Phe Val Gln Ala Leu Cys Ser Ile Leu Asn Glu His			
248	275	280	285	
249	ggc aag gac ctc gag atc atg cag atc ctg acc agg gtg aac gac agg	1388		
250	Gly Lys Asp Leu Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg			
251	290	295	300	305

**VERIFICATION SUMMARY**

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